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score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

### OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 00:16:08 ; Search time 4340.53 Seconds  
(without alignments)  
10982.631 Million cell updates/sec

Title: US-09-001-737-7\_COPY\_15\_1652  
perfect score: 1638  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 204640 seqs, 1451402878 residues  
Total number of hits satisfying chosen parameters: 4109280  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenBank:  
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3: qb\_in:  
4: qb\_cm:  
5: qb\_ov:  
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7: qb\_ph:  
8: qb\_pl:  
9: qb\_pr:  
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12: qb\_st:  
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14: qb\_vl:  
15: en\_ba:  
16: en\_fun:  
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23: en\_pat:  
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25: en\_pj:  
26: en\_ro:  
27: en\_sts:  
28: en\_vl:  
29: en\_vt:  
30: en\_htg\_hum:  
31: en\_htg\_inv:  
32: en\_htg\_other:  
33: en\_htg\_mus:  
34: en\_htg\_pln:  
35: en\_htg\_rod:  
36: en\_htg\_mam:  
37: en\_htg\_vrt:  
38: en\_sy:  
39: en\_htgo\_hum:  
40: en\_htgo\_mus:  
41: en\_htgo\_other:

Pred. No. is the number of results predicted by chance to have a

### SUMMARIES

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C 2	1605.8	98.0	53291 AE01470	AE01470 Streptoco
C 3	1605.8	97.8	11576 AE010115	AE010115 Streptoco
C 4	1413.4	86.3	2683 1 SPGRDOLGN	XN9236 S progenes
C 5	1413.4	86.3	2683 6 AX148805	AX148805 Sequence
C 6	1170.4	71.5	1421 1 AF121365	AF121365 Streptoco
C 7	1404.4	69.6	1306 6 AX148006	AX148006 Sequence
C 8	1128.8	68.9	1421 1 AX121364	AX121364 Streptoco
C 9	1125	68.7	1422 1 AX121366	AX121366 Streptoco
C 10	1122.5	68.5	1415 1 AF121367	AX121367 Sequence
C 11	1118	68.3	1415 1 AF121367	AF121367 Streptoco
C 12	1104.2	67.4	2054 1 AF389314	AF389314 Streptoco
C 13	1080	65.9	1384 1 AF121363	AY121363 Streptoco
C 14	1075.4	65.7	2324 1 AF389516	AF389516 Streptoco
C 15	1068.2	65.5	2320 1 AF389515	AF389515 Streptoco
C 16	1063.6	64.9	2020 1 AF389517	AF389517 Streptoco
C 17	1052.8	64.3	178 1 AF32922	AF32922 Streptoco
C 18	1050.4	64.1	2639 1 AF378195	AF378195 Streptoco
C 19	1050.4	64.1	2750 1 AF378196	AF378196 Streptoco
C 20	1039.4	63.4	1623 6 AX194119	AX194119 Sequence
C 21	1038.4	63.4	1926 6 AX07550	AX07550 Sequence
C 22	1037.6	63.3	21494 2 SPNEUJ924	SPNEUJ924 Sequence
C 23	1036	63.2	1647 1 AX194338	AX194338 Sequence
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C 25	1036	62.9	2107 1 AF32449	AF32449 Streptoco
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C 35	947.8	57.7	12671 1 ALGROESL	X71132 L. lactis gr
C 36	942	57.5	3120 1 AF335185	AF335185 Enterococ
C 37	941.4	57.5	217 1 AF102215	AY039215 Lactococc
C 38	844.6	51.6	2831 1 AB073399	AB073399 Tetragen
C 39	839.4	51.2	2834 1 AB02452	AB02452 Bacillus
C 40	837.8	51.1	2309 1 BACILLOR	L10132 Bacillus st
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### ALIGNMENTS

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DEFINITION Streptococcus pyogenes ML GAS strain SF370, section 156 of 157 of the complete genome.  
VERSION AE006627\_AE004092  
KEYWORDS  
SOURCE Streptococcus pyogenes ML GAS.  
ORGANISM Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
Strptococcus.  
REFERENCE 1 (bases 1 to 10389)  
Ferretti,J.J., McHan,W.M., Adjic,D., Savic,G., Lyon,K.,  
Prineaux,C., Sezate,S.S., Surorov,A.N., Kenton,S., Lai,H., Lin,S.,  
AUTHORS



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AEO14170/c  
**LOCUS** AE014170 Streptococcus pyogenes MGAS315, section 35 of 37 of the complete genome  
**DEFINITION**  
**ACCESSION** AE014170 AE014074  
**VERSION** AE014170.1 GI:21905475  
**KEYWORDS**  
**SOURCE** Streptococcus pyogenes MGAS315.  
**ORGANISM** Streptococcus pyogenes MGAS315.  
**REFERENCE** Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
**AUTHORS** Beres,S.B., Sylva,G.L., Barbán,K.D., Lei,B., Hoff,J.S.,  
 Mamarella,N.D., Liu,M.-Y., Smoot,J.C., Porcella,S.F.,  
 Parkins,L.D., McCormick,J.K., Leung,D.Y.M., Schlievert,P.M. and  
 Musser,J.M.  
**TITLE** Genome sequence of a serotype M3 strain of group A Streptococcus:  
 Phage-encoded toxins, the high-virulence phenotype, and clone  
 emergence  
**JOURNAL** Proc. Natl. Acad. Sci. U.S.A. 99 (15), 10078-10083 (2002)  
**REFERENCE** 2 (bases 1 to 53291)  
**AUTHORS** Beres,S.B., Sylva,G.L., Barbán,K.D., Lei,B., Hoff,J.S.,  
 Mamarella,N.D., Liu,M.-Y., Smoot,J.C., Porcella,S.F.,  
 Parkins,L.D., McCormick,J.K., Leung,D.Y.M., Schlievert,P.M. and  
 Musser,J.M.  
**FEATURES** Direct Submission  
**JOURNAL** Submitted (14-JUN-2002) Laboratory of Human-Bacterial Pathogenesis,  
 Rocky Mountain Laboratories, NIAID, NIH, 903 South Fourth St.,  
 Hamilton, MT 59840, USA  
**source** Location/Qualifiers  
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AEO14170  
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**DEFINITION**  
**ACCESSION** AE014170 AE014074  
**VERSION** AE014170.1 GI:21905475  
**KEYWORDS**  
**SOURCE** Streptococcus pyogenes MGAS315.  
**ORGANISM** Streptococcus pyogenes MGAS315.  
**REFERENCE** Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
**AUTHORS** Beres,S.B., Sylva,G.L., Barbán,K.D., Lei,B., Hoff,J.S.,  
 Mamarella,N.D., Liu,M.-Y., Smoot,J.C., Porcella,S.F.,  
 Parkins,L.D., McCormick,J.K., Leung,D.Y.M., Schlievert,P.M. and  
 Musser,J.M.  
**TITLE** Genome sequence of a serotype M3 strain of group A Streptococcus:  
 Phage-encoded toxins, the high-virulence phenotype, and clone  
**JOURNAL** Proc. Natl. Acad. Sci. U.S.A. 99 (15), 10078-10083 (2002)  
**REFERENCE** 2 (bases 1 to 53291)  
**AUTHORS** Beres,S.B., Sylva,G.L., Barbán,K.D., Lei,B., Hoff,J.S.,  
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gene  
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CDS

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REFERENCE	1 (bases 1 to 2683)		
AUTHORS	Wright, J.A., Young, A.H. and Dugourd, D.		
TITLE	Antisense oligonucleotide sequences derived from groel and groes as inhibitors of microorganisms		
JOURNAL	Patent No. 031635 A7 25-MAY-2001; GenSense Technologies Inc. (CA)		
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ORGANISM	Bacterium, Firmicutes; Lactobacillales; Streptococcaceae;		
VERSION	AY121365.1	GI:22022469	
KEYWORDS	Streptococcus dysgalactiae subsp. equisimilis.		
SOURCE	Streptococcus dysgalactiae subsp. equisimilis.		
ORGANISM	Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;		
REFERENCE	Stræptococcus		
AUTHORS	Woo, P.-C.Y., Teng, J.L.L., Lau, S.K.P., Lum, P.N.L., Leung, K.-W., Tsui, H., Wong, K.-L., Li, K.-W., Lam, K.-C. and Yuen, K.-Y.		
TITLE	Chaperonin GroEL gene of Group G Streptococcus dysgalactiae subspecies equisimilis		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1421)		
AUTHORS	Woo, P.-C.Y., Teng, J.L.L., Lau, S.K.P., Lum, P.N.L., Leung, K.-W., Tsui, H., Wong, K.-L., Li, K.-W., Lam, K.-C. and Yuen, K.-Y.		
JOURNAL	Pokfulam Road, Hong Kong, China		
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Best Local Similarity	89.0%		
Matches	1264		
Conservative	0		
Mismatches	156		
Indels	0		
Gaps	0		
Qy	71 ATACCGCAAGTAACGCTGTTGCTCAAAGGCGCATSTGTTCTGAAAGCTT	130	
Db	1 ACACGGTAAAGTACGCTGTTGCTCAAAGGCGCATSTGTTCTGAAAGCTT	60	
Qy	131 GTCTCCCTAACTACTATGAGGGTAACTATCTAAAGATGCAATTAGAGTC	190	
Db	61 GATCTCTTGTACCATGAGGGTAACTATGCTAAAGATGCAATTAGAGTC	120	
Qy	191 ATTGGAACATGGCAAAATGGCTCTGAGCTGGCTCAAACCAAGATATTG	250	
Db	121 ATTGGAATGGACTAAATGGCTTCTGAACTTGTCTTAAACCAAGATATG	180	
Qy	251 CTGGTGTGGGACACTCTGCAACAGTTTCACAAAGCCATCTGCAAGGATCA	310	
Db	181 CAGGTGGGACCAACTCTGCAACAGTTTCACAAAGCCATCTGCAAGGATCA	240	
Qy	311 AAATGGAACGGGCTATCCAACTGGTATCGTGGGACGACAGCACAG	370	
Db	241 AACATGAACTCTGGTCCACCCAAATTGGTATTGTTGTTGGGATGAAACAGCACAG	300	
Qy	371 CAACAGGTGGTGAAGCCATGTCACCTGTATCTGGCAAGGAGCTT	430	
Db	301 CAACAGCGCTGAGCTGTTGAGCTTGTCTGTTCTGTTGAGCGATG	360	
Qy	431 CTGGGCTGCGTCACTGATCATACCGCTGTAAGAAGTTGGAGTATCTCAGANGCA	490	
Db	361 CTCAAGTTGCTGCTGTCATCTGGTTGAAAGTGTGGAGATCACCTCGAGCCA	420	
Qy	491 TTGAGCTGGGGCAAGGATGGTGTGATTACATGGAGATCTCGAGGTTAGAAGAC	550	
Db	421 TTGAACTGTGGCAATGACGGTCACTTACATGGAGATCACCGTGTGTTAGAGCA	480	
Qy	551 ACTTGAGCTGGTGAAGCATGGTCAATTGACCGCTTACCTGTCATATGCA	610	
Db	481 AGCTTGAGCTGGTGAAGCATGGTCACTTACCTGTCATATGCA	540	
Qy	611 CAGACATGAAATGGTGCAGACCTGAAACCCATTATCTTAATCAGGATAAA	670	
Db	541 CAGACATGAAATGGTGCAGACCTGAAACCCATTATCTTAATCAGGATAAA	600	
Qy	671 ACTGTGCAACATCCAAGACATTGCCACTTGAGCTTCTTAACACCGTC	720	
Db	601 ACTGTGCAACATCCAAGACATTGCCACTTGAGCTTCTTAACACCGTC	650	
Qy	731 CATTACTCATATTGAGCATGGTGGGACTCTCAACCCCTGCTGAC	790	
Db	661 CATTACTCATATTGAGCATGGTGGGACTCTCAACCCCTGCTGAC	720	
Qy	791 AGATGTGCTACTTCATGTTGCTGTCAGAACGCCAGATTTGTGTGTCGCTGA	850	
Db	721 AGATGTGCTACTTCATGTTGCTGTCAGAACGCCAGATTTGTGTGTCGCTGA	780	
Ov	R51 AGCTTGTGAGCTGAGCAGGCTGCTGTCAGAACGCCAGATTTGTGTGTCGCTGA	810	





Db	1261	CCTGTCGTCAAATGCATCAACGCTGGTTACAGAGTCCGGTTMCACAAATGA	1320	Db	121	AATATGGAGCTAAATGTTCTGAACTTCTAAACCAATGATCGCAGGTGAC	130
Oy	1400	AAACAGCCTCAGAACAGGTTAATCCTGCAACAGGGTACTGGTTCATGATA	1459	Oy	259	GGACGCTACTSCAACAGTTTACACAGGCTATGTCACAGGCTATGTCAGGACTTAAATGTG	318
Db	1321		1380	Db	181	GGACCAACTGCAACTGAGATTTGACACAGGTATGTCGGTAAGGGCTTAAATGTG	240
Oy	1460	AAACGGATTCTGACCTGTCAGAAGCTTAACTGCACAGTGATGGTAGATG	1499	Oy	319	ACGAGCTGCTAACTCATGGATCGTGGAGGATGAAACGCAACGCAACGCT	378
Db	1381	CGGAGGTTATTATCGATCCGTAAAGTAACCCGTTACAG	1420	Db	241	ACTCGTGTGCCAACCTATGGTATGGTGTGGATGAGCACACGCAACGCT	300
RESULT	9			Db	241	ACTCGTGTGCCAACCTATGGTATGGTGTGGATGAGCACACGCAACGCT	300
AY121366				Db	301	GTGAGGCTCTGAAGCTATGCTCAGCCATGCTGAAAGAATGGAGATGAC	438
DEFINITION				Oy	439	GTCGACATATGTCACCTGTCACCTTATGTCAGAAGCTTGGAGCT	498
ACCESSION				Db	361	GTCGCTGTCTGCTCTGAAAGAATGGAGATGACATCTCGAAGAACGCT	420
VERSION				Oy	499	GTGGCACCTGTGATTCACATCGAAGATCTCGAGGATGAAACGACTGAA	558
KEYWORDS				Db	421	GTGGCACATACGTCATACCTGACATGTCAGGATGACAGCTGAA	440
ORGANISM				Oy	559	GTGGTGTGGCTGCAATGACCGTGTACCGTCTCACATGTCAGACAT	618
REFERENCE				Db	481	GTGTTGAGGAGCAGTCAGCTGCTGTTGACCGTGTACCTGTCACAGACAT	540
AUTHORS				Oy	619	GAAAATGTTGCGACCTGAAACCAATTAACTTAACACGATAAAAGCTA	678
TITLE				Db	541	GAAAATGTTGCGACCTGAAACCAATTATCTGATRACTGACAAAGCTA	600
JOURNAL				Db	679	AACATCCAGACATTGCTCACTACTGAGGAGTCTAAACCAACCGTCATACTC	728
UNPUBLISHED				Db	601	ACATCCAGATTTCCCACTACTTGAGGAGTCTAAACCAACCGTCATACTG	660
1 (bases 1 to 1422)				Oy	739	ATTATCGACATATGCGGTTGAGCTGACCGCTGCTGACAGATCTG	798
Koo, P. C. Y., Teng, J. L. L., Lau, S. K. P., Lum, P. N. L., Leung, K. -W.,				Db	661	ATTATCGCGATACGTTGATGCGGAGCTTCCAAACCTTGTTGATAAATGCTG	720
Tse, H., Wong, K. -L., Li, K. -W., Lam, K. -C. and Yuen, K. -Y.				Oy	799	GTCATCTATGCTGTCAAAGGCCAGATTGTCAGCTGTAAGCTAC	858
TITLE				Db	841	TGAAANGACCTACATGCCAGCTCTGGCAAGCCGTTAAGCTGCTGAA	900
DIRECT SUBMISSION				Oy	979	ACACAGTATTCATGCTGTCAGAGCTGTCAGCTAACGCTTGGCT	1038
SUBMITTED (12-JUN-2002)				Db	901	ACGACAGTATTCGAGGAGTCAGGAGTCAGCAACGCCAAGCTGTC	960
MICROBIOLOGY, The University of Hong Kong,				Oy	1039	ATTAAACCGATTAACAAACCTGACTGACCTGACCTGAAACCTAAGACCT	1098
Pokfulam Road, Hong Kong, China				Db	961	ATTAAGTCACACTAGACACACTCTGAAATTGATGACCC	1020
LOCATION/QUALIFIERS				Oy	1059	TGGCATATTACTGCTGCTGCTGCTGATCAAGTAGGAGCTCAACAGAGCT	1158
SOURCE				Db	1021	TTGGCAATTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1080
1. (1422 bases)				Oy	1159	TGAAAGAATGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1218
/organism="Streptococcus dysgalactiae subsp. equisimilis"				Db	1081	CTAARGAAATGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1140
/strain="CIP 55-123"				Oy	1219	GAAGTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1278
/sub_species="equisimilis"				Db	1141	GAAGTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1200
/db_xref="GI:2202492"				Oy	1279	CTTGAGCTGAGGGCATATGCTGCTGCTGCTGCTGCTGCTG	1338
/product="chaperonin GroEL"				Db	1201	CTTGAGCTGAGGGCATATGCTGCTGCTGCTGCTGCTGCTG	1260
/protein_id="PAM83129_1"							
/transl_table=11							
/codon_start=1							
ORIGIN							
BASE COUNT	407	a 278 c 354 g 383 t					
QUERY MATCH	68.7%	Score 1125; DB 1; Length 1422;					
BEST LOCAL SIMILARITY	87.0%	Pred. No. 8.7e-220; Matches 125; Conservative 0; Mismatches 185; Indels 0; Gaps 0;					

QY	1339	CCGTGAGCTAACATTGCTTAAATCCTGGTAGGAGGTCCTTAATTGACATTG	1398
Db	1261	CCGTGAGCTAACATTGCTTAAATCCTGGTAGGAGGTCCTTAATTGACATTG	1320
QY	1399	AAAACAGGCCCTGGAGAACGCGATTGAACTTGTCAACAGGTGAGGGTTGATATT	1458
Db	1321	AAAATAGCCCTGGAGAACGCGATTGAACTTGTCAACAGGTGAGGGTTGATATT	1380
QY	1459	AAAACAGGAACTCATGGCCCTGGAGAACGCGATTGAACTTGTCAACAGGTGAGC	1499
Db	1381	GGCGCAGGTTATNCATCCCTGTTAAGTAACCGCTCAGC	1421
RESULT	10		
LOCUS	AX148809		
DEFINITION	Sequence 11 from Patent WO0136625.		
ACCESSION	AX148809		
VERSION	1		
KEYWORDS			
SOURCE	Streptococcus pyogenes.		
ORGANISM	Streptococcus pyogenes		
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;			
Streptococcus			
REFERENCE			
AUTHORS	Wright,J.A., Young,A.H. and Dugourd,D.		
TITLE	(bases 1 to 1305) Antisense oligonucleotide sequences derived from groEL and groES as inhibitors of microorganisms		
JOURNAL	Patent: WO 0136625-A1 25-MAY-2001; GenSense Technologies Inc. (CA)		
FEATURES			
source	1..1305		
BASE COUNT	406 a 238 c 312 g 349 t		
ORIGIN			
Query Match			
Best Local Similarity	68.5%	Score 1122.6;	DB 6;
Matches	1128;	Length 1305;	Pre. No. 2.7e-21;
	Conservative	0;	Mismatches 9;
		Indels 0;	Gaps 0;
QY	489	TATGGAGCTTGCGAACATGCTGATACATCGAGAGATCGAGGATGGAAC	548
Db	1	TATGGAGCTTGCGAACATGCTGATACATCGAGAGATCGAGGATGGAAC	60
QY	549	AAAGTTGAGTTGTAAGGCATGCAATTGACCGTGTACCTCTCAATACATGG	608
Db	61	AAAGTTGAGTTGTAAGGCATGCAATTGACCGTGTACCTCTCAATACATGG	120
QY	609	CACAGACAATGAAATAGTTCAGACCTTGAACCCATTACTTATACGATAA	658
Db	121	CACAGACAATGAAATAGTTCAGACCTTGAACCCATTACTTATACGATAA	180
QY	669	AAAGTGCAACATCCAAGCATTTGCACTACTTGTGGCTTAAACCAACCG	728
Db	181	AAAGTGCAACATCCAAGCATTTGCACTACTTGTGGCTTAAACCAACCG	240
QY	729	TCCATTACTATATGCGACATATGCGATGATGCGACACTTGTGGCTTAAACCAACCG	788
Db	241	TCCATTACTATATGCGACATATGCGATGATGCGACACTTGTGGCTTAAACCAACCG	300
QY	789	CGAGATCGTGTGACTTCATGGCTGTAACGCCAGATTGGATGGATGCTG	848
Db	301	CGAGATCGTGTGACTTCATGGCTGTAACGCCAGATTGGATGGATGCTG	360
QY	849	AAACCTCTGCTGAGACATTGCACTTGACAGTGTACAGGATACAGGATC	908
Db	361	AAACCTCTGCTGAGACATTGCACTTGACAGTGTACAGGATACAGGATC	420
QY	909	AGAGCTTGATTAAGAGCTGCTCAAGACGCCCTGGACGGTGTCAAGTACG	988
Db	421	AGAGCTTGATTAAGAGCTGCTCAAGACGCCCTGGACGGTGTCAAGTACG	480
RESULT	11		
LOCUS	AY121367		
DEFINITION	Streptococcus dysgalactiae strain HKU 7 chaperonin GroEL gene, Partial cds.		
ACCESSION	AY121367		
VERSION	1		
KEYWORDS			
SOURCE	Streptococcus dysgalactiae.		
ORGANISM	Streptococcus dysgalactiae		
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;			
Streptococcus			
REFERENCE			
AUTHORS	(bases 1 to 115)		
TITLE	Woo,P.C.Y., Teng,J.L.L., Lau,S.K.P., Lum,P.N.L., Leung,K.-W., Tse,H., Wong,R.-L., Lin,W., Lam,K.-C. and Yuen,K.-Y.		
JOURNAL	Chaperonin GroEL gene of Group G Streptococcus dysgalactiae		
REFERENCE	Unpublished		
AUTHORS	(bases 1 to 1415)		
TITLE	Woo,C.Y., Teng,J.L.L., Lau,S.K.P., Lum,P.N.L., Leung,K.-W., Tse,H., Wong,R.-L., Lin,W., Lam,K.-C. and Yuen,K.-Y.		
JOURNAL	Submitted (12-JUN-2002) Microbiology, The University of Hong Kong, Pokfulam Road, Hong Kong, China		
FEATURES			
source	1..1415		
/strain="streptococcus dysgalactiae"			

BASE COUNT	404	276	c	353	9	382	t
<b>ORIGIN</b>							
Query Match	68.3%	Score	1118	DB 1:	Length	1415	
Best Local Similarity	86.9%	Pred No.	2,3e-218				
Matches	1229;	Mismatches	185;	Indels	0;	Gaps	0;
Qy	86	CGCTTGGCTTAAGGGCCHATGTTGTCCTGAAGAACCTTGTGTCCTTA 145					
Db	1	CGCTTGGCTTAAGGGCCHATGTTGTCCTGAAGAACCTTGTGTCCTTA 60					
Qy	146	CTATGAGGGGGTACCTTGCTTAAGAGATGAGTTAGAGTCATTGAAACTGG 205					
Db	61	CCATGAGGGGGTACCTTGCTTAAGAGATGAGTTAGAGTCATTGAAACTGG 120					
Qy	206	GACCAAAATGGTCTGCAAGTGCTCTAAACCAATGATATTGGGGATGGAGA 265					
Db	121	GACCAAAATGGTCTGCAAGTGCTCTAAACCAATGATATTGGGGATGGAGA 180					
Qy	266	CTACTGCAACAGTTGACAAACGATGTTGCAAGAGCTAAATGACACCG 325					
Db	181	CTACTGCAACAGTTGACAAACGATGTTGCAAGAGCTAAATGACACCG 240					
Qy	326	GTGCTTAATCCAAATGGTATCGGGCATGATGAAACGACGACAGCGTGCAG 385					
Db	241	GTGCCAACCCAAATGGTATGGTGGGATGAAACGACGACAGCGTGCAG 360					
Qy	385	CTCTGAAAGGCATGTCGAACCTTATGCAAGAAGACTTGTCTGCGTCAG 445					
Db	301	CTCTGAAAGCTATGGCTCACGCTTTCGGTAAAGACCGATGTCAGTGCCTG 460					
Qy	446	TATCATCACGCCCTGAAACATGAGAGTATOTCGAGACCTTGTGGCGTGGCA 505					
Db	361	TGTCATCTCTCTGAAAAGTGGAGATACATTCAGAACGCCCTGGACGGTGGCA 420					
Qy	506	ACCATGTTGATACCTGCAAGRAATCTCGAGGATGAAACAGACTTGAAAGTGTG 565					
Db	421	ATGACCGGTGTCATTCACATCGAAATCACGGTGGATGGACAGCTGGTAG 480					
Qy	566	AGGCATGCAATTGACCGGTGTCATACATGTCACAGAACGATGAAAGAAAA 625					
Db	481	AGGCATGCAATTGACCGGTGTCATACATGTCACAGAACGATGAAAGAAAA 540					
Qy	626	TGTTGCAAGCTCTGAAACCAATTACTTAACTCAGCGATAAAAGCTGAACTC 685					
Db	541	TGTTGCAAGCTCTGAAACCAATTACTTAACTCAGCGATAAAAGCTGAACTC 600					
Qy	686	AGGCATGTTGCAAGCTCTGAAACCAATTACTTAACTCAGCGATAAAAGCTGAACTC 745					
Db	601	AGGCATGTTGCAAGCTCTGAAACCAATTACTTAACTCAGCGATAAAAGCTGAACTC 660					
Qy	746	CAGATGATGTTGGTGAAGCACTTCACCAACCTTGTGTGACAGAAAGTCTGGCACT 805					
Db	661	CAGATGATGTTGGTGAAGCACTTCACCAACCTTGTGTGACAGAAAGTCTGGCACT 720					
Qy	805	TAATGTGGTGTGCAAGCCGAGATTGGTGTGCAAGTGTGAAAGTGTGCACT 865					
<b>RESULT</b> 12							
AF389314	AF389314	2054 bp	DNA	linear	BCT	02-JUL-2002	
LOCUS	AF389314	Streptococcus bovis	Gross gene,	complete	cds;	and	GroEL gene,
DEFINITION		Streptococcus bovis	partial	cds.			
ACCESSION	AF389314	Streptococcus	Streptococcus				
VERSION	AF389314.1	GI:21666288					
KEYWORDS							
SOURCE		Streptococcus bovis.					
ORGANISM		Streptococcus bovis					
JOURNAL		Streptococcus	Firmicutes;	Lactobacillales;	Streptococaceae;		
REFERENCE		Streptococcus					
AUTHORS		1 (bases 1 to 2054)					
REFERENCE		Teng,J.-J.					
JOURNAL		The groESL genes of Streptococcus bovis					
TITLE		Unpublished					
REFERENCE		2 (bases 1 to 2054)					
AUTHORS		Teng,J.-J.					
TITLE		Direct Submission					
JOURNAL		Submitted (08-JUN-2001) School of Medical Technology, National					
FEATURES		Taiwan University of Medicine, No. 1, Chang Te Street,					
source		Taipei 100, Taiwan					
		Location/Qualifiers					
		1. 2054					
		/organism="Streptococcus bovis"					
		/db_xref="taxon:1315"					



VERSION	AY121363.1	GI	22202485
REFERENCE	Streptococcus dysgalactiae subsp. dysgalactiae.		
SOURCE	Streptococcus dysgalactiae subsp. dysgalactiae.		
ORGANISM	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococci.		
AUTHORS	Woo, P.C.Y., Teng, J.L.L., Lau, S.K.P., Lum, P.N.L., Leung, K.-W., Tse, H., Wong, R.-L., Li, K.-W., Lam, K.-C. and Yuen, K.-Y.		
TITLE	Chaperonin GroEL gene of Group C Streptococcus dysgalactiae subspecies dysgalactiae		
JOURNAL	Unpublished manuscript		
REFERENCE	2 (bases 1 to 1384)		
AUTHORS	Woo, P.C.Y., Teng, J.L.L., Lau, S.K.P., Lum, P.N.L., Leung, K.-W., Tse, H., Wong, R.-L., Li, K.-W., Lam, K.-C. and Yuen, K.-Y.		
TITLE	Direct Submission		
JOURNAL	Submitted (11-JUN-2002) Microbiology, The University of Hong Kong, Pokfulam Road, Hong Kong, China		
FEATURES	Location/Qualifiers		
source	1..1384 [organism="Streptococcus dysgalactiae subsp. dysgalactiae" /strain="ATCC 43078" /sub_species="dysgalactiae" /db_xref="ATCC:43078" /db_xref="taxon:99822" /cl: >1384 /codon_start=3 /transl_table=11 /product="chaperonin GroEL" /protein_id="AAW83126.1" /db_xref="GI:2202486"]		
CDS			
BASE COUNT	397 a 269 c 349 g 369 t ORIGIN		
Query Match	65.9% Score 1080; DB 1; Length 1384;		
Best Local Similarity	86.3%; Pred. No. 1.4e-210;		
Matches	1194; Conservative 0; Mismatches 190; Indels 0; Gaps 0;		
OY	104 GCAATGTTGTCTTGAAAGCTTGTGGTCCTTAATTCTAATGAGCGGTAAACCA 163		
OY	1 GTATGTTGTCTTGAAAGCTTGTGGTCCTTAATTCTAATGAGCGGTAAACCA 60		
OY	164 TTGCTTAAGAGCATGCAATTAGAGAACATTTGAAACAGTGGAGCAAAATTGGTGTG 223		
OY	61 TTGCTTAAGAGCATGCAATTAGAGAACATTTGAAACAGTGGAGCAAAATTGGTGTG 120		
OY	224 AAGGGCTCTAACACCATGATATGCTGGTGTGGAGACTACGACACTTTGAA 283		
OY	121 AAGTGTCTAACACTAACATGATATGCTGGTGTGGAGACTACGACACTTTGAA 180		
OY	284 CACAGGCGATGTTCTACATGAAAGCTGACAGCACGCTGAA 343		
OY	181 CACAGGCTATGTTCTGTTGAAAGTGTGAACTGCTGCAACCCATTGCA 240		
OY	344 TGTGTCAGGCTGAACAGCACAGCACGCTGAAACGCTGAAGCATTGCTC 403		
OY	241 TTGCTCTGGGATGAGCACGAGCACGCTGAA 300		
OY	404 AACCTGTTGCAAGCTATGCTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 463		
OY	301 AGCTGTTGTCGCTAACAGAACGCTATGTCAGTCAGTCAGTCAGTCAGTC 360		
OY	464 AAGTGGAGACTATCTCAGAGSTATGGAGCTGGCTGAGCTGTTATTCACCA 523		
RESULT	REF0514		

LOCUS	AF189516	2324 bp	DNA	linear	BCT 02-JUL-2002
DEFINITION	Streptococcus mutans GroES gene, complete cds; and GroEL gene, partial cds.				
ACCESSION	AF189516				
VERSION	1				
KEYWORDS	Streptococcus mutans				
ORGANISM	Streptococcus mutans				
BACTERIA; Firmicutes; Lactobacillales; Streptococcaceae;					
STREPTOCOCCUS; Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;					
1 (bases 1 to 2324)					
TENG, L.-J.					
Direct Submission					
Submitted (08-JUN-2001) School of Medical Technology, National Taiwan University College of Medicine, No. 1, Chang-Te Street, Taipei 101, Taiwan					
FEATURES					
SOURCE					
Unpublished					
2 (bases 1 to 2324)					
Teng, L.-J.					
Direct Submission					
Submitted (08-JUN-2001) School of Medical Technology, National Taiwan University College of Medicine, No. 1, Chang-Te Street, Taipei 101, Taiwan					
REFERENCE					
AUTHORS					
TENG, L.-J.					
The groES genes of Streptococcus mutans					
JOURNAL					
Unpublished					
2 (bases 1 to 2324)					
Teng, L.-J.					
Direct Submission					
Submitted (08-JUN-2001) School of Medical Technology, National Taiwan University College of Medicine, No. 1, Chang-Te Street, Taipei 101, Taiwan					
CDS					
Location/Qualifiers					
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LTKKISNTODPVLPEVAKRNPILLIADQDVEGAUPLTMNLNTRGIFNVAKA					
PGFDRRKMLDEDAVUGVTTIDEDGELKDUTDQGARQVWVNDKSTVRS					
GGKEAVANVRNLTKSQETATSDFRDLKQEVYVAKVATELKEM					
RIDLALMTRAWEVGIVTAGGAGTTLNQVYVNLVRALEPPIQ					
TANAGCSEGVTIDKLNSAGTETENANGWVNDIDAGIUDPVRVTSALQNSAWA					
SLLTMTTAAVPAHPPAPEAPAHAPNDES"					
ORIGIN					
BASE COUNT					
695 a					
368 c					
544 g					
717 t					
Query Match	65.7%	Score 1075.4;	DB 1:	Length 2324;	
Best Local Similarity	79.8%	Pred. No. 1.1e-209;			
Matches 1268; Conservative	0;	Mismatches 321;	Indels 0;	Gaps 0;	
QY	1	ATGCCAAGAACCAAACTATTTCGCGAGATCGCGCTATGCGCCATTGCGGAGTGAT	60		
Db	717	ATGCCAAGAACCAAACTATTTCGCGAGATCGCGCTATGCGCCATTGCGGAGTGAT	776		
QY	61	ATTTTACAGATTCGGCAAGTGTACCGCTTGTCTTAAGGCCCATGTTGCTTGATGAA	120		
Db	777	ATTTTACAGATTCGGCAAGTGTACCGCTTGTCTTAAGGCCCATGTTGCTTGATGAA	120		
QY	121	AAAGCTTGTGTCCTTAATCTACTATAGCGGGTACCATTCATAAGAGATGCAA	180		
Db	837	AACTCGTTGGTCACGGCTCATTAATCTATAGCTGGTACCATCTAAAGA	895		
QY	181	TTGAGATGATTTGAAACATGGGACAAATTGGCTCTGAAGCTGGCTTAAACC	240		
Db	897	TTGAGATGATCTGAAATATGGGACCTAAAGCTGGCTTCAAGTGTCAAGTAAACT	956		
QY	241	ATGAGATGCTGGTGGACCAACTACTGACACAGTTGACACAACCATTTGTCAT	300		
QY					
Db	957	AATGATATTCGCCGTGATGSGACACGACCACTGCTGTTACTCAGCTATGCTG	1016		
QY	301	GAAGGCTAAATGTCGACGCGGCTTATCAATGTTATCGCTGCAGGCATGAA	360		
Db	1017	GAAGGTGAAATGTCGCTGAGCTACCCAAATGTTATCGCTGCAGGAATGCA	1076		
QY	361	ACAGCACACACAGCTGTTGAGGCCTGAAACCATGCTTACCTGACTCGCAAG	420		
Db	1077	ACAGCAGTTCACAGGATGTTGAGCTGTTGAAAGTGGGATGCACTGCGCTG	1136		
QY	421	GAAGCTTCTCTGGTGCAGTACGTTGAGCTGTTGAAAGTGGAGATPATAC	480		
Db	1137	GAAGCTTGTGACAGGTTGAGCTGTTGAAAGTGGGATGCACTGCGCTG	1256		
QY	541	ATGGAAACAGAACTTGAGCTGTTGAGCTGTTGAAAGTGGGATACCTGCTCA	600		
Db	1257	ATGGAAACAGAACTTGAGCTGTTGAGCTGTTGAAAGTGGGATACCTGCTCA	1196		
QY	601	TGAGACTTGTGAGCTGTTGAAAGTGGTGTGAACTCATGAGAAAGTGGAGAT	540		
Db	1197	TGAGACTTGTGAGCTGTTGAAAGTGGTGTGAACTCATGAGAAAGTGGAGAT	1256		
QY	661	ACGGATAAAACTGCAACATCAGAATTGTCACACTGTTGAGCTGTTGAAAGT	720		
Db	1317	TATATGTTACTGACATGAAAAATGTCGAGCTGTTGAGAAATCTTATGTTAATT	1376		
QY	721	ACCCAGCTTCACTCTTATGCTGAGATGTTGAGCTACTGTTGAGCTTAA	780		
Db	1437	ACAGATAGAAATTTCATGAAATTCAGAGTTGAGCTGTTGAGAAATCTTATGTTAATT	1436		
QY	781	GTCTTGACAAAGTGTGCTACTTCATGTCGTTCTGCAAGGCCAGATTGT	840		
Db	1497	GTGTTGATAAGATGTTGTTGTTACTTCATGTTGTCGAGCTGAGGCTCCTGTTGCTG	1556		
QY	841	GATCGTTGAAAGCCATGTTGAGATGTTGCTGAGCTATGTCAGCTGTTGAGCTCAGCTTACA	900		
Db	1557	GTGTCGCCAAAGCCATGTTGAGATGTTGCTGTTTACAGGGGACTCTGTT	1616		
QY	901	GAGGATCTGGACTGTTGAAATTAAGAGATGCTTACATGACACCCCTGAGCAGCTGCTAAG	960		
Db	1617	GGAGTCCTGGCTAGATGAAAGTACCACTATGTTGAGCTGTTGAGCTCAGCAGCTGT	1676		
QY	961	ATTTACAGTTGATAGATGCACTGTTGAGCTGTTGAGCTGTTGAGCTGTT	1020		
Db	1677	GGAGTCCTGGCTAGATGAAAGTACCACTATGTTGAGCTGTTGAGCTGTT	1736		
QY	1021	GTCATACGGTATGACTGTTAATGCAATTAGAACACAACTTGTGCTGTT	1080		
Db	1737	GCTAAATCTGTCACATCTTAACTGTCATGAACTGACCACTGCTGTT	1795		
QY	1081	GAAGACCTGAGAGCTTGGGAATTGCTGTTGTTGAGCTGTTGAGCTGTT	1140		
Db	1797	GAAGAAATTCACAGAACGGTTGGCTTAATTTATCTGGAGGTTGTCGCRCAATGTTG	1856		
QY	1141	GTCCTCAAAGACAGACGCTTAAAGAAATGAACTTGGCATTTGAGGTTCTAATGCT	1200		
Db	1857	GCAGAACAGACGACGCTTAAAGAAATGAACTTGGCATTTGAGGTTCTAATGCT	1916		
QY	1797	ATGAAAGTAGAGACGAACTGTTGAGCTGTTGAGCTGTTGAGCTGTT	2036		
QY	1201	ACACCTGGAGCGCTGGAGCTGTTGAGCTGTTGAGCTGTTGAGCTGTT	1650		
Db	1917	ACTGGAGCTGTTGAGCTGTTGAGCTGTTGAGCTGTTGAGCTGTT	1976		
QY	1261	ATGGAAAGTAGAGCTGTTGAGCTGTTGAGCTGTTGAGCTGTTGAGCTGTT	1916		
Db	1977	ATGAAAGTAGAGCTGTTGAGCTGTTGAGCTGTTGAGCTGTTGAGCTGTT	2036		
QY	1221	CTTCGTGCTGAGAGCCCTGAGCTGTTGAGCTGTTGAGCTGTTGAGCTGTT	1380		
Db	2037	CTGGCTGCTGAGAGCCCTGAGCTGTTGAGCTGTTGAGCTGTTGAGCTGTT	2096		

		Matches 1268; Conservative 0; Mismatches 333; Indels 0; Gaps 0;
OY	1381 GTAGTTATGACAGTGGAAACAGCTCAGAACAGGTTAATGCTGAGAGT 1440	OY 1 ATGCCAAGAAGTAATCAATTTCAGCAGTGCGCCTGCCTCCATGGCGGGAGTGT 60
Db	2097 GTCATTTGATGATATGAGAACAGTCAGCAGCTACGGTCACTCGGG 2156	Db 719 ATGCCAAGAAGTAATCAATTTCAGCAGTGCGCCTGCCTCCATGGCGGGAGTGT 778
OY	1441 GACTGGGTGATGATGATGAAAGGATCATTCACCCCTCAAGTAACGAGCAGG 1500	OY 61 ATGTTACAGATACCGTAAAGTAACGCTGTCCTAAGGGCAATGTTCTGGA 120
Db	2157 GATGGGTGACATGATGATGATGGGATTAATCTGTCAGAGTGTGAGCTG 2216	Db 779 ATTATGAGATACGGTAAAGTAACGCTGTCCTAAGGGCAATGTTCTGGA 120
OY	1501 CTCAAATGCACTCTGATGAGTAAAGGATCATTCACCCCTCAAGTAACGAGCAGG 1560	OY 121 AACCTTGTGTCCTTAATCTATGAGGGTACCATTSCTAAAGATGGA 180
Db	2217 CTCAAATGCACTCTGATGAGTAAAGGATCATTCACCCCTCAAGTAACGAGCAGG 2276	Db 839 AATCATTTGCTCACCTCATCACAAATGAGGGTACATTTGCGCAAGAATGGA 898
OY	1561 AAACCTGACCCACTGCCAGGCCAGC 1589	OY 181 TTGAAATCTGTTGAGAACATGGGAGAAATGTTGCTGAACTGGGTTCAAGAATGGA 240
Db	2277 CATCCAGCTCAGAAGCACCAGCAGCAGC 2305	Db 899 CTCGAATATCATTGAAATATGGCCCTAAGTGGTCTGAAATGGAAT 958
RESULT 15		OY 241 AATGATATGCTGTGATGGAGCTACTGGCAACAGTTGACACAGCTTCAAGTGTCTCAAAC 958
AF389515		Db 959 AATGATATGCTGTGATGGAGCTACTGGCAACAGCTTCAAGTGTCTCAAAC 958
DEFINITION	AF389515 2320 bp DNA linear BCT 02-JUL-2002	Db 1079 ACAGCTTGCACAGCTTGAATGAGCTTAAAGCAATTCCTGTCAGTTGTC 300
ACCESSION	Streptococcus intermedius GroES gene, complete cds; and GroEL gene, partial cds.	OY 301 GAAGGACTAAATAATGACAGCAGGTTCAATCCAAATGTTACGGTTCAGTGA 360
VERSION	AF389515.1 GI:21666291	Db 1019 GAAGGACTCAAAATGTTACGGCTGTCGACACCAATGTCATGCTGTTGATGAA 1078
KEYWORDS	Streptococcus intermedius.	OY 361 ACAGCAACACAGAGCTGTCACCTGTCACCTGTCACCTGTCACCTGTCACCTGTCAC 420
ORGANISM	Streptococcus intermedius.	Db 1139 GAMGCGATTCGACAAAGTGTGCGTGTTCACAGCTCTGAAAATGCGGATAC 1198
BACTERIA	Firmicutes; Lactobacillales; Streptococcaceae;	OY 481 TCGAGACCTGAGGCTGGGAAAGTAGTGTGAAATGACATGGCTGACCTGGTACCTGGCTCA 540
STREPTOCOCCUS	1 (bases 1 to 2320)	Db 1199 TCTGAAGCCATGGAAAGTGTGCAACAGAGCTGTCACATATGAGAAATGCGGATAC 1198
REFERENCE	Teng,L.-J. The groESL genes of Streptococcus intermedius Unpublished work (bases 1 to 2320)	OY 541 ATGGAAACAGACTGAGGCTGGGAAAGTAGTGTGAAATGACATGGCTGACCTGGTACCTGGCTCA 600
AUTHORS	Teng,L.-J	Db 1259 ATGGAAACAGACTGAGGCTGGGAAAGTAGTGTGAAATGACATGGCTGACCTGGTACCTGGCTCA 1318
JOURNAL	Submitted (08-JUN-2001) School of Medical Technology, National Taiwan University College of Medicine, No. 1, Chang-Te Street, Taipei 100, Taiwan	OY 601 TACATGTCACAGACATGAAATGGCTGACCTGTGAAACCCATTTCATTC 660
FEATURES	Location/Qualifiers	Db 1319 TACATGTCACAGACATGAAATGGCTGATGAAATTCATTCATTC 660
SOURCE	1..2320 <organism>"Streptococcus intermedius" <db_xref>taxon:1338"	OY 661 AGGGATAAAAGTGCACACATCCAGAACATTGGCACACTGAGTTGGCTCA 720
CDS	405..686	Db 1379 ACAGATAGAAATTCATACCGAACATTCCTTGTGGAAATTTTAA 1438
	/codon_start=1	OY 771 ACCACACGTCATCTACTCTATATGCGATGATGTGTGAACTTCACCCCT 780
	/transl_table=11	Db 1439 ACAACTGCGCCATTGTGATGAGGATGATGAGCTTCACCTCT 1498
	/product="GroES"	OY 781 GCTTGACACATGTTGACTTCATGCTGCTGCTGCTGACGCCAGGTTG 840
	/protein_id="AMT3643_1"	Db 1499 GTGTTGACACATGTTGACTTCATGCTGCTGCTGACGCCAGGTTG 840
	/db_xref="GI:21666292"	OY 841 GATGCTCTAAGCTGATGTTGAGACATGCTATGCTGAGGTGAGTGTACA 900
	/translation="MADKIFSAARSAMVRQDILADTVKUTLGPKGRNVVLEKSF	Db 1559 GACCTCTTAAAGCTGATGAGCTGACCTGTTGCGTACAGCTGCTGAA 1618
	SPLITNGVIAKEIIEDEHFNNGAKLVSEVAKTNDIAGGTTATLTVTAIYREG	OY 901 GAGGTCTAGACTGAAATGCTGATGAGCTGCTGAGCTGCTGAGCTGCTG 960
	IKNVTAGANFIGRRGTTGATTAATVAKLNSVPSNEAIAQVIAVSSRSKVEYI	Db 1619 GAGGTCTGCTGATGAGCTGACCTGAGCTGACCTGCTGAGCTGCTG 1678
	SEAMEKVGNDGVTIESKNDPTEVYEGHOFGRGYLSQMVNTNEWADNRYI	OY 961 ATTACAGTGTGATGATGAGCTAATGTTGAGGTTGAGAATTCAGAGCTT 1020
	LITDKTKINTOFLPLLENLTKSPILLADDVGENPLVLUKIGFIVAWKA	Db 1679 GAACTGCGGATAAGACGACCCATTGCTGAGGGCTGCTGAGCTGCTG 1738
	PERGDERKAMLEDDIPLGTTEDGCLERDTIELAGQSKVVKDSDVTEGS	OY 1021 GCTAACCTGATGACTGATGAAATGCTGCAATGAAACACACTCTGACTTGACCGT 1010
	GDKARAVKRSQESTVSEDFDKERDLAKLSSGAVVKGAAATEPELKKML	Db 1739 GCTAACCCGCTGCTGCTAAATGCAAACTGCTGATGCTGCTG 1798
	ILANACFPESSIVDRKLNSEVGGTAPVNUVDAVLAELFADATGNTVRLAEEPVRO	
	SILITPEAVVAAASOPERAAPAMDPS"	
BASE COUNT	731 a 408 c 527 g 654 t	
ORIGIN		
Query Match	65.2%; Score 1068.2; DB 1; Length 2320;	
Best Local Similarity	79.2%; Pred. No. 3.2e-208;	

QY	1081	GAAACTACAGAACGTTGGCAAATATGCGTGTGGTAGCTGTATCAAGTAGGA	1140
Db	1799	GAAGAACATACAGAACGTTGGCAAATATGCGTGTGGTAGCTGTATCAAGTAGGT	1858
Qy	1141	GTCACAGACGACTTAAGAATGAACTTCAGATGCGATGAGGTGCTTAATGCT	1200
Db	1859	GTCACAGACGAGAACGAACTCAAGAATGAACTTCAGATGAGGTGCTTAATGCA	1918
Qy	1201	ACAGCTGCAGCGTGTGAGAAGGTATCGTGTGGTGAGAAGAGCTATTCAGTT	1260
Db	1919	ACTGTCGCGCTGTGAGAAGAATGTCAGGTTGGAACAGCTTGTGTATGTT	1978
Qy	1261	ATTGAAAGAACGAGGAGCTTGAGCTGAGCTGAGGCGAGATGAGGAGCTGAGC	1320
Db	1979	TAGATGCACTGGCGCTTGACGTTGGAGGCTGATGAGCAACAGGTCGCAATTG	2038
Qy	1321	CTCGCTGCTAGAGAACCTTGTAGTCATAATGCTTAATGCTGGTAGAAGGCRC	1380
Db	2039	CTCGTGTCTGGAGAACCTTGTAGTCATAATGCTGGTAGAAGGCRC	2098
Qy	1381	GTAGTATGCACTGGAAACAGCCGTGAGGACAGGATTAACTGTCACACGGT	1440
Db	2099	ATGCTCATGACCGTTGAAACACTCTGTGAGTGTGAGATGATTAATGCTGCACATGCG	2158
Qy	1441	GAGGGTTGATGATTAACAGAACGAACTATGACCCGTCAAGAACGATGCG	1500
Db	2159	GATGGCTTACAGATGAGCAGGGATCATGACCCACTCACTGCTGCG	2218
Qy	1501	CTTCAAAATGCGCTGACTGTCTATTTGACACAGAACGAGCTGCTAT	1560
Db	2219	CTTCAAAATGCGCTGCTGAGTGTGCTGCTGCTATTTAACACAGAACGAGCTG	2278
Qy	1561	AACCTGACAGCTAGCCAGCGCAGAATGCCAGCAG 1601	
Db	2279	CAACAGAACGCTAGCCAGCTCCGCAATGATCCAG 2319	